Assignment of Y-chromosomal SNPs found in Japanese population to Y-chromosomal haplogroup tree

Type: Article

Abstract:
The relationship between Y-chromosome single-nucleotide polymorphisms (SNPs) registered in the Japanese SNP (JSNP) database (http://snp.ims.u-tokyo.ac.jp) and Y-binary haplogroup lineages was investigated to identify new Y-chromosomal binary haplogroup markers and further refine Y-chromosomal haplogroup classification in the Japanese population. We used SNPs for which it was possible to construct primers to make Y-specific PCR product sizes small enough to obtain amplification products even from degraded DNA, as this would allow their use not only in genetic but also in archeological and forensic studies. The genotype of 35 JSNP markers were determined, of which 14 were assigned to appropriate positions on the Y-chromosomal haplogroup tree, together with 5 additional new non-JSNP markers. These markers defined 14 new branches (C3/64562 + 13, C3/2613-27, D2a1b/006841*, D2a1b/119166-11A, D2a/022456*, D2a/119166-11A, D2a/119167rec/119167-40rec*, D2a/75888-GC, O3a3c/075888-9T/10T*, O3a3c/075888-9T/9T, O3a3/8425 + 6, O3a3/119166-13A*, O3a3/008002 and O3a4/037852) and 21 new internal markers on the 2008 Y-chromosome haplogroup tree. These results will provide useful information for Y-chromosomal polymorphic studies of East Asian populations, particularly those in and around Japan, in the fields of anthropology, genetics and forensics.

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